Hoelzer, G., Drewes, R. & Doursat, R. (2006) Temporal waves of genetic diversity in a spatially explicit model of evolution: Heaving toward speciation. *6th International Conference on Complex Systems (ICCS 2006)*, June 25-30, 2006, New England Complex Systems Institute (NECSI), Boston, Massachusetts.

Temporal waves of genetic diversity in a spatially explicit model of evolution: heaving toward speciation

Guy Hoelzer¹, Rich Drewes² & René Doursat^{2,3}

¹Department of Biology/314, ²Brain Computation Laboratory/400 ³Department of Computer Science and Engineering/171 University of Nevada, Reno, Reno NV 89557, USA

Abstract—A commonly held view in evolutionary biology is that speciation, i.e., the emergence of genetically distinct and reproductively incompatible subpopulations, is generally driven by external geographical boundaries. We have developed a spatially explicit model of a biological population to study the emergence of spatial and temporal patterns in genetic diversity in the absence of predetermined domains. We propose a 2-D cellular automata model showing that an initially homogeneous population might spontaneously segment into different species through sheer isolation by distance. The model includes sexual individuals as agents, with diploid genomes comprised of two autosomal chromosome pairs. Each location on the lattice can contain several such individuals, which follow simple rules relating to their mutation, reproduction and migratory dispersal. Each chromosome is a sequence of 1000 nucleotide bases (GATC) subjected to mutation (base substitution) at rate μ . We have not allowed for crossing over within chromosomes, but non-homologous chromosomes assort independently during sexual recombination. Individuals are hermaphrodites able to function as either the male or female in a sexual encounter. The mean reproductive rate in the population is regulated each generation to buffer swings in population size resulting from a variety of factors, such as stochastic mortality. The model shows an inherent tendency toward spatial self-organization, as has been the case with other spatially explicit models of evolution. Each generation we assess the genetic difference between pairs of randomly chosen individuals and plot a frequency histogram of these differences (the mismatch distribution) to explore the non-spatial pattern of genetic diversity in the population. A well-mixed version of the model exhibits a relatively stable and unimodal distribution of genetic differences as has been shown with previous models. However, a much more interesting pattern of temporal waves emerges when the dispersal of individuals is limited to short distances. Each wave represents a subset of comparisons between members of emergent subpopulations diverging from one another. The long-term persistence of diverging subpopulations is the essence of speciation in biological populations, so the rhythmic diversity waves we have observed suggest an inherent tendency for such a population to generate new species.